



Relationship between genetic diversity of *Chenopodium quinoa* and the dynamics of its seed exchanges in Chile

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Introduction:

Quinoa cultivation in Chile presents an ancient and active complex of geographic, climatic, social and cultural interactions that has determined its current biodiversity in the three main growing zones (north, centre and south). These interactions consider a central issue viz. the participation of farmers, whose activities are at the base of seed exchanges networks due to their knowledge and *in situ* conservation of genetic diversity. In this study we report antecedents that contribute to a better understanding of seed exchanges through the analysis of field works assessing the key roles of farmers involved in the biodiversity dynamics and characterization of 20 microsatellites genetic markers in a multi-origin set of 34 representative quinoa accessions of Chile and South American region.

Materials and methods

Study area:

- North¹ (Tarapaca) /Aymara culture/altitude: 3500 masl/18–22°S/annual precipitation 100-200 mm.
- Centre² (O'Higgins)/isolated farmers/altitude: 100-200 masl/34–36°S/ annual precipitation 500-800 mm.
- South³ (Araucania)/Mapuche culture/altitude: 50-600 masl/37–39°S/annual precipitation: 2000 mm

Fieldwork documentation:

- 2008 season: semi-directed interviews; 21 in north, 13 in centre, and 5 in south.
- 2009 season: 92 polls and interviews; 31 in north, 26 in centre, and 35 in south.
- Multiple factor analysis of information using Statistica 6.0[®] Software.

Genetic Analysis:

- 34 quinoa accessions provided by institutional seed Banks.
- 20 di/tri-nucleotide loci microsatellites used by Fuentes *et al.* (2009).
- A pairwise matrix using Jaccard's similarity coefficient (FreeTree[®]); UPGMA cladogram computed after 500 replicates for bootstrap test (Tree View Win32 ver1.6.6. software); Heterozygosity values (TFPGA software, version 1.3), Comparison of polymorphic nucleotide motifs (unpaired Student's *t*-test; $P \leq 0.05$ / INFOSTAT statistical software).



Results and discussion

Genetic analysis

- 118 polymorphic markers for all accessions (mean alleles per locus = 5.90).
- Tri-nucleotide loci motif were significantly more polymorphic than two-nucleotide motifs (*t*-test; $P \leq 0.05$).
- *H* mean value of 0.65, suggests a wide genetic diversity sampled as well as the good informative quality of markers (60% highly polymorphic) (Table 1).
- UPGMA analysis yielded two major groups, subdivided into five population (Figure 1).

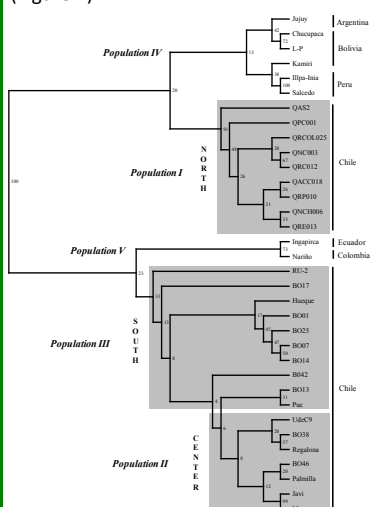


Figure 1. UPGMA cladogram based on Jaccard's similarity. Gray rectangles represent the main growing areas of quinoa in Chile.

- The populations were consistent with classification described by Risi and Galwey (1984) and production zones focused in this study.

Table 1. *H* and Wright's F_{ST} -statistics values for each locus microsatellite.

Locus microsatellite	GenBank accession n°	N° of alleles	<i>H</i> value	F_{ST} †
1 KGA16	DQ462130	4	0.64	0.61
2 QAAT24	DQ462136	8	0.84	0.24
3 QCA48	AY458240	4	0.61	0.52
4 QAAT74	DQ462141	8	0.79	0.39
5 QCA24	DQ462151	6	0.63	0.56
6 KGA20	DQ462131	5	0.70	0.37
7 QAAT70	DQ462139	7	0.74	0.23
8 QCA120	DQ462156	4	0.30	0.39
9 QCA88	DQ462154	2	0.40	0.02
10 QGA17	DQ462158	4	0.12	0.17
11 QCA57	AY458243	6	0.80	0.43
12 QGA02	DQ462157	7	0.76	0.33
13 QAAT50	DQ462137	8	0.74	0.37
14 QAAT78	DQ462143	7	0.80	0.27
15 QCA38	DQ462152	8	0.79	0.30
16 KGA003	DQ462129	5	0.70	0.33
17 QATG86	DQ462147	4	0.51	0.35
18 QAAT76	DQ462142	11	0.87	0.04
19 QCA14	DQ462150	4	0.42	0.33
20 QCA37	AY458227	6	0.81	0.23
Mean		5.90	0.65	0.33

† Nei (1978).

† Wright's F_{ST} statistics value (Wright, 1951).

Assessment of fieldwork documentation

- The different handling of the production system by farmers have generated diversity of biodiversity in quinoa (Table 2).

Table 2. Principal variables describing the local farming system of quinoa.

Variable	North	Centre	South
i Number of producers	> 170	> 70 [†]	> 50 [†]
ii Hectares	1374	130 [†]	10 [†]
iii Production (ton)	801.8	100 [†]	2.9
iv Grain yield (kg ha ⁻¹)	580	978	1074
v Mean number of landraces per field crop	3-5	1	1-3
vi Photoperiod sensibility of landraces	Insensible	Sensible	Sensible
vii Growth period	August-May	September-April	October-March

i, ii, iii and iv: information from 2007 National Agricultural Census (INE, 2007) completed and corrected by fieldworks (*minimum estimation).

- Farmers are the main actors of the biodiversity conservation.

- There is two types of exchanges representing the main access to seeds: individual (inside communities) and collective (local markets).

- The definition of variety is given mainly by colour of the panicle. A sub-classification is made by size and shape of plants.

Conclusions

- The genetic information allowed the detection of variation among and within population, which did match well with natural geographical-edaphic-climatic constraints to the expansion of quinoa biodiversity.

- The grouping correlated well with the social-linguistic context of ancient people inhabiting the Andes region, where agronomic and cultural traditions kept until present days show large differences.

- Risks to biodiversity in this species are postulated due to small scale of farmers.

References

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